

Figure 1A

10 30 50
 GCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCCGCGCCGTGGGCAGGTGCT
 70 90 110
 GAGCGCCCCCTAGAGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGACAT
 130 150 170
 GGGGTGTTGGAGGTAGATGGGCTCCCCGCGGGAGGCGGCGGTGGATGCGGCGCTGGGC
 190 210 230
 AGAAGCAGCCGCGGATTCCAGCTGCCCCGCGCGCCCCGGGCGCCCCCTGCGAGTCCCCGGT
 250 270 290
 TCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATCGCC
 M G T S P S S S T A L A S C S R I A
 310 330 350
 CGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCTTAGCACC
 R R A T A T M I A G S L L L L G F L S T
 370 390 410
 ACCACAGCTCAGCCAGAACAGAAGGCCTCGAATCTCATTGGCACATACGCCCATGTTGAC
 T T A Q P E Q K A S N L I G T Y R H V D
 430 450 470
 CGTGCCACCGGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTCTCTGAG
 R A T G Q V L T C D K C P A G T Y V S E
 490 510 530
 CATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGGGGACCTTTACCAGG
 H C T N T S L R V C S S C P V G T F T R
 550 570 590
 CATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATGATT
 H E N G I E K C H D C S Q P C P W P M I
 610 630 650
 GAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCCACCTGGCATGTTG
 E K L P C A A L T D R E C T C P P G M F
 670 690 710
 CAGTCTAACGCTACCTGTGCCCCCATAACGGTGTGCTGCTGCGGGTACCTTCTCAGAT
 Q S N A T C A P H T V C P V G W G V R K
 730 750 770
 AAAGGGACAGAGACTGAGGATGTGCGGTGTAAGCAGTGTGCTCGGGGTACCTTCTCAGAT
 K G T E T E D V R C K Q C A R G T F S D
 790 810 830
 GTGCCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGTCTGAGTCAGAACCTGGTG
 V P S S V M K C K A Y T D C L S Q N L V
 850 870 890
 GTGATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCCTTCTCC
 V I K P G T K E T D N V C G T L P S F S
 910 930 950
 AGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACC
 S S T S P S P G T A I F P R P E H M E T
 970 990 1010
 CATGAAGTCCCTTCTCCACTTATGTTCCCAAGGCATGAACTCAACAGAATCCAACCTCT
 H E V P S S T Y V P K G M N S T E S N S

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2025

1990	2010	2030
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I F D D M L H F L N P E E L R V I E E I		
2110	2130	2150
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P Q A E D K L D R L F E I I G V K S Q E		
2170	2190	2210
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A S Q T L L D S V Y S H L P D L L *		
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2350	2370	2390
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2410	2430	2450
TTCTCTCTCTCTTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCC		
2470	2490	2510
AGGTGTAAGTGTGTGAAATACCCACCCTAAAGTTTTTTAAGTTCCATATTTCTCCAT		
2530	2550	2570
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2590	2610	2630
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2650	2670	2690
TAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTCACACCTACTT		
2710	2730	2750
TTTAAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAAATTTCTTAAA		
2770	2790	2810
GATTAAGAAAATTTAAGACCCCATTTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCT		
2830	2850	2870
TTTAAATATGTCTTGTATAGTTTCATATTCATGGCTGAAACTTGACCACACTATTGCTGAT		
2890	2910	2930
TGTATGGTTTTTCACCTGGACACCGTGTAGAATGCTTGATTACTTGTACTCTTCTTATGCT		
2950	2970	2990
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3010	3030	3050
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3070	3090	3110
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3190	3210	3230
CCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCTTTCACCAATTACTTTAATTAAA		
3250	3270	3290
AATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAA		

Figure 1D

3310	3330	3350
ATGTACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTG		
3370	3390	3410
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3430	3450	3470
ACTAATTTATTAATAAACATTAGGTGTTTGTTAAAAAAAAAAAAAAAAAAAAA		

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Figure 2

1 MGIWT ---LLPLVLT SVARLSSKSVHAQVTDINSKGLLEL ---RKTVTTPETQNLLEGLHHDDGOF -CHKP h Fas
1 M-GAGATGRA ---M DGPRLLLELLLGVSLLGGAKAEACPTT GLYTHSGEC ---CKA h NGR p75
1 M-GUSTVPDLLLLLPLEVLEL -LVGIYPSGVIGLVPHLGDRE -KRDSVCPOGKYIH -PQNSI -CCTK h THER I
1 M-GTSPSSSTALASCSRIARRATATMIAGSLLELJGFLSTTTAQPEQKASHLI GTYRH VDRATGOVLTCDK TR9

63 CPGERKARDCTVNGDPPDCVPCQEGKEYTDKAHFSKCRKRCL -CDEGHGGLLEVEIH -CTRQTQMTKCRCK h Fas
47 CHLGEVQAQPCG -ANQTVCEPCCLDSVTFSDVVSATPECPCTE -C -VGLQSMASPCVADAVCRCA h NGR p75
62 CHKGTLYLWDCPGPGQDTCRECESGS -PTASENHLRHCLSCSK -CKR KENG -QVEISSCTVDRDTVCGGR h THER I
70 CPA GT-YVSEHGT -HTSLRVCS -PVGTFTRHENGIEKCHDCSQPC -PVPMIIEKLPCAAALTDEGCTCP TR9

131 PU ---F FCHN ---STVC ---EH ---CDPCTKC -EHGI - - h Fas
111 YGYQ ---DETTGRCEACRVCEAGSLVFSCQDKQNTVCEECPDGTYSDEAHNVDPCLPCTVC -EDTERQ h NGR p75
129 KHQYRHYWSENLFQCFNCSLCLNG -TVHLSCQEKONTVCT -CHAGFEFRENE - -C VSGSNG -KKS LEC h THER I
135 PGMFQ ---SHAT -CAPHTVCPVGVGRKKGTETEDVVRCKQCARGTFSNDVPSSVMHKKAYTDCLSQNLVV TR9

154 IREC -TLTSHIT --- ---KCKEEGSRSHL --- --- h Fas
177 LRECTRWADAECBEIPIGRWITRNTPTDEGSDSTAFTQEPAPPEQDLIASTVAGVVTVMGSSQPVVTRG h NGR p75
192 TRLELPQIENV --- ---KGTEDSGTTLPL - - - - h THER I
200 INPGTKETDNVCGTLPSESSSTRPSPGTATFPPEHMETHEVPSTYVPKGMNSTESHSSARVPKVLSS TR9

175 --- ---GWL -C ---LL -LPLJ --- --- h Fas
247 TTDNLITVYCRILAAVVVGLVAYIAFKRWNSCKONKQGANRPVHQTIRPEGEKLSHSDSGISVDS - - - h NGR p75
216 --- ---LVIFPG -L -C --- ---LSSLLEFI - - - - h THER I
270 IQEGTVPDHTSSARGKEDVNKTLPNLQV - -VNHQCGPHRHILKLETPSM EATGTGEKSSPTIKGPKRGH TR9

185 ---PLIV ---EVQKTCRKHKE - -NQGSHESPQ ---LWPE - - h Fas
312 ---QSLUDQ -QPHQTQA - - -SGQALK - - -GDGLYSSLPAPKRE h NGR p75
231 ---GLMYRYOR - - -W -RSK - - -LYSIVCGKSTPE - -KEGELEGTIT - -KPLAPUPS - h THER I
336 PRQHLHKEHEDIUEHLPMHIVLFLLVLVIVVCSTIRKSSRTLRKKGPRQDPSAIVEKAGLKKSMPTPTQURE TR9

219 ---TVAINLSDVDLSKYIT - - - - -T --- h Fas
347 ---VEKLLHGSAGDTWRHLAGELGYQPEH - - -IDSETHAFCPVRRALLASWATQDS -ATL h NGR p75
273 ---FSPTPGFTPLGFSVPVPSSTETS - - - - -SSTYTPGDGCPNFAA - - - h THER I
406 KWIYYCNGHGDPLKTLVAAQVGSQMKDIYQFTICNASEREVAAPFSGYTDADHERAYAAALQHTTIRGPEASL TR9

236 --- ---IAGVMTLSQV --- --- h Fas
399 DALALRLRIQRADLVESL - - - - - --- h NGR p75
310 ---PRREVAPPYQG - - - - -ADPILATALASDEIPHLQKWEDESAHKKPSLDTPDP h THER I
476 AOLISALRQHRNDVVEKIRGLMEDTTQLETDKLALPHSPSPSPSPSPSHNAKLENSALLTVEPSQDK TR9

246 --- ---KGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRHMHQLHGKKEA -YDTLIKULK h Fas
418 --- ---CSE ---STATSP - - - - - h NGR p75
357 ATLYAVVEHVPPLRWKEFPVRLGLSDHEDLELQHGRCLEAQYSMHATMRRTTPRREATLELGRVJR h THER I
546 NKGFFVDESEPLLRCD - - - - -TSSGSSALLSRNGSFITKEKKDVTLRQVRLDPCDLQPIFDMLHFLN TR9

300 KANLECTLAERKQTI - - - - -ILKNDTSDSENSEN - - - - -FRNEIQSLV h Fas
427 DMDDL LGCLEDEEAA - - - - -L - - - - -CGPAA - - - - -LPPAPSLLR h NGR p75
609 PEEL -RVIEEIPQAEKDDRLLFEITGVKRSQEAASQTLLDSVYSHLPDL - - - - - h THER I
TR9

Figure 3

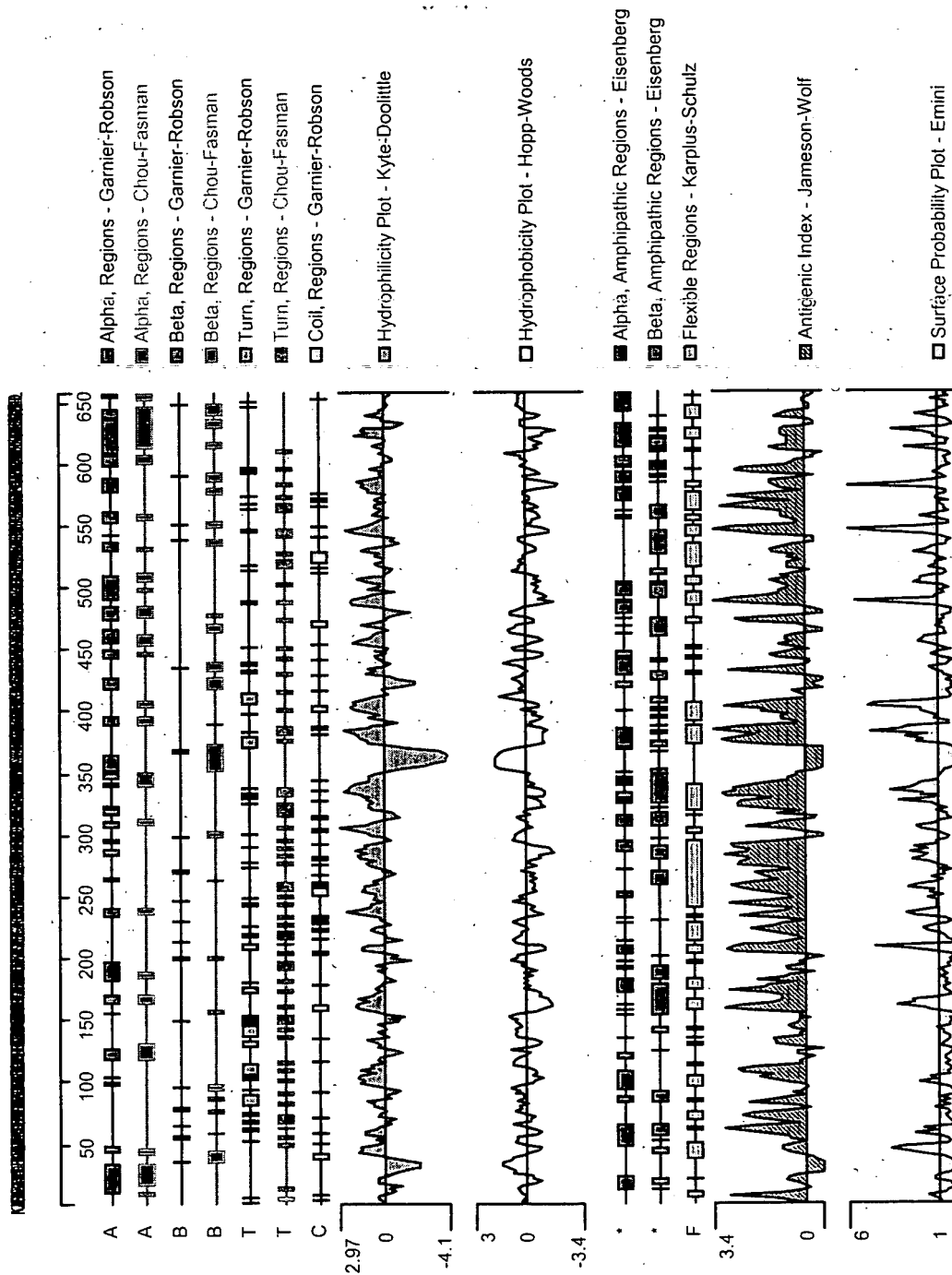


Figure 4A

1 MGTSPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKC 70
PAGTYVSEHCTNTSLRVCCPCVGTFTRHENGIEKCHDCSQPCWPWMIKLPAAALTDRECTCPPGMFQS 140
NATCAPHTVCPVGWGVRRKKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNV 210
CGTLPFSSTSPSPGTAIFPRPEHMETHEVPSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
SARGKEDVNKTLPNLQVVNHQQPHRHILKLLPSMEATGGEKSSTPIKGPKRGHPQNLHKHFDINEHL 350
PMMIVLELLLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILK 420
LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLISALRQHRNDV 490
VEKIRGLMEDTTQLETDKLALPMSPLSPSPISPSPNAKLENSALLTVEPSPQDKNKGFVDESEPLLR 560
DSTSSGSSALSRNGSFITKEKKDVTVLQRVRLDPCDLQIFDDMLHLFNPEELRVIEEIPQAECLKDLRLE 630
IIGVKSQEASQTLSDSVYSHLPDLL 655

[illegible]

TR9
CD95
TNFR1
DR3
DR4
DR5

Figure 5

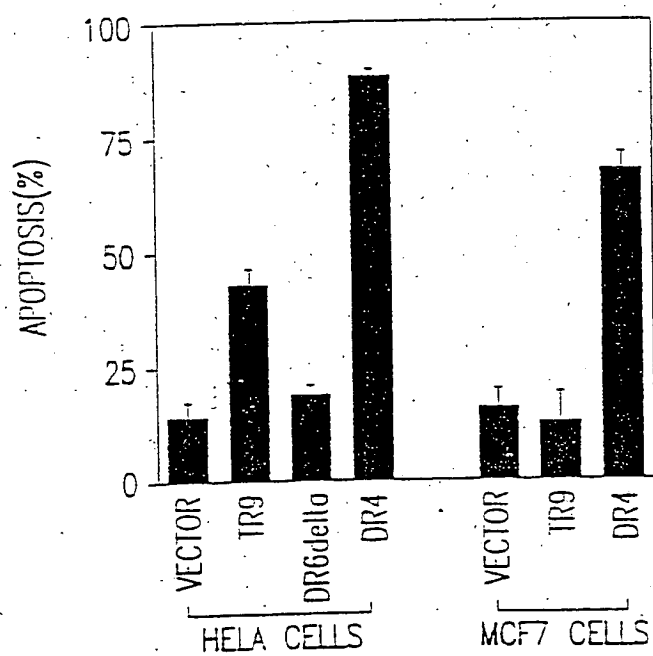


Figure 6

